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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/073,138

DATE: 07/25/2002

TIME: 14:33:23

Input Set : N:\Crf3\RULE60\10073138.raw

Output Set: N:\CRF3\07252002\J073138.raw

ENTERED

SEQUENCE LISTING

- 3 (1) GENERAL INFORMATION:
- 5 (i) APPLICANT: ANDERSON, Darrell R.
- 6 HANNA, Nabil
- 7 BRAMS, Peter
- 9 (ii) TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING
- 10 INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN
- B7.1 AND B7.2 CO-STIMULATORY ANTIGENS
- 11
- 13 (iii) NUMBER OF SEQUENCES: 6
- 15 (iv) CORRESPONDENCE ADDRESS:
- 16 (A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
- 17 (B) STREET: P.O. Box 1404
- 18 (C) CITY: Alexandria
- 19 (D) STATE: Virginia
- 20 (E) COUNTRY: United States
- 21 (F) ZIP: 22313-1404
- 23 (v) COMPUTER READABLE FORM:
- 24 (A) MEDIUM TYPE: Floppy disk
- 25 (B) COMPUTER: IBM PC compatible
- 26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- 27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- 29 (vi) CURRENT APPLICATION DATA:
- C--> 30 (A) APPLICATION NUMBER: US/10/073,138
- C--> 31 (B) FILING DATE: 13-Feb-2002
- 32 (C) CLASSIFICATION:
- 34 (vii) PRIOR APPLICATION DATA:
- 35 (A) APPLICATION NUMBER: US/08/746,361
- 36 (B) FILING DATE: 08-NOV-1996
- 38 (A) APPLICATION NUMBER: US 08/487,550
- 39 (B) FILING DATE: 07-JUN-1995
- 41 (viii) ATTORNEY/AGENT INFORMATION:
- 42 (A) NAME: Teskin, Robin L.
- 43 (B) REGISTRATION NUMBER: 35,030
- 44 (C) REFERENCE/DOCKET NUMBER: 012712-256
- 46 (ix) TELECOMMUNICATION INFORMATION:
- 47 (A) TELEPHONE: (703) 836-6620
- 48 (B) TELEFAX: (703) 836-2021
- 51 (2) INFORMATION FOR SEQ ID NO: 1:
- 53 (i) SEQUENCE CHARACTERISTICS:
- 54 (A) LENGTH: 705 base pairs
- 55 (B) TYPE: nucleic acid
- 56 (C) STRANDEDNESS: single
- 57 (D) TOPOLOGY: linear

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59      (ii) MOLECULE TYPE: DNA (genomic)
61      (ix) FEATURE:
62          (A) NAME/KEY: CDS
63          (B) LOCATION: 1..705
65      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
67 ATG AGG GTC CCC GCT CAG CTC CTG GGG CTC CTG CTG CTC TGG CTC CCA      48
68 Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp Leu Pro
69   1           5           10           15
71 GGT GCA CGA TGT GCC TAT GAA CTG ACT CAG CCA CCC TCG GTG TCA GTG      96
72 Gly Ala Arg Cys Ala Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val
73           20           25           30
75 TCC CCA GGA CAG ACG GCC AGG ATC ACC TGT GGG GGA GAC AAC AGT AGA      144
76 Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asp Asn Ser Arg
77           35           40           45
79 AAT GAA TAT GTC CAC TGG TAC CAG CAG AAG CCA GCG CGG GCC CCT ATA      192
80 Asn Glu Tyr Val His Trp Tyr Gln Gln Lys Pro Ala Arg Ala Pro Ile
81   50           55           60
83 CTG GTC ATC TAT GAT GAT AGT GAC CGG CCC TCA GGG ATC CCT GAG CGA      240
84 Leu Val Ile Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg
85  65           70           75           80
87 TTC TCT GGC TCC AAA TCA GGG AAC ACC GCC ACC CTG ACC ATC AAC GGG      288
88 Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Thr Leu Thr Ile Asn Gly
89           85           90           95
91 GTC GAG GCC GGG GAT GAG GCT GAC TAT TAC TGT CAG GTG TGG GAC AGG      336
92 Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg
93           100           105           110
95 GCT AGT GAT CAT CCG GTC TTC GGA GGA GGG ACC CGG GTG ACC GTC CTA      384
96 Ala Ser Asp His Pro Val Phe Gly Gly Gly Thr Arg Val Thr Val Leu
97           115           120           125
99 GGT CAG CCC AAG GCT GCC CCC TCG GTC ACT CTG TTC CCG CCC TCC TCT      432
100 Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
101           130           135           140
103 GAG GAG CTT CAA GCC AAC AAG GCC ACA CTG GTG TGT CTC ATA AGT GAC      480
104 Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
105 145           150           155           160
107 TTC TAC CCG GGA GCC GTG ACA GTG GCC TGG AAG GCA GAT AGC AGC CCC      528
108 Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
109           165           170           175
111 GTC AAG GCG GGA GTG GAG ACC ACC ACA CCC TCC AAA CAA AGC AAC AAC      576
112 Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
113           180           185           190
115 AAG TAC GCG GCC AGC AGC TAC CTG AGC CTG ACG CCT GAG CAG TGG AAG      624
116 Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
117           195           200           205
119 TCC CAC AGA AGC TAC AGC TGC CAG GTC ACG CAT GAA GGG AGC ACC GTG      672
120 Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
121           210           215           220
123 GAG AAG ACA GTG GCC CCT ACA GAA TGT TCA TGA      705
124 Glu Lys Thr Val Ala Pro Thr Glu Cys Ser *
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W--> 125 225                230                235
128 (2) INFORMATION FOR SEQ ID NO: 2:
130 (i) SEQUENCE CHARACTERISTICS:
131 (A) LENGTH: 1431 base pairs
132 (B) TYPE: nucleic acid
133 (C) STRANDEDNESS: single
134 (D) TOPOLOGY: linear
136 (ii) MOLECULE TYPE: DNA (genomic)
138 (ix) FEATURE:
139 (A) NAME/KEY: CDS
140 (B) LOCATION: 1..1431
142 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
144 ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCT CCC AGA TGG      48
145 Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
W--> 146                240                245                250
148 GTC CTG TCC GAG GTG AAG CTG CAG CAG TGG GGC GAA GGA CTT CTG CAG      96
149 Val Leu Ser Glu Val Lys Leu Gln Gln Trp Gly Glu Gly Leu Leu Gln
W--> 150                255                260                265
152 CCT TCG GAG ACC CTG TCC CGC ACC TGC GTT GTC TCT GGT GGC TCC ATC     144
153 Pro Ser Glu Thr Leu Ser Arg Thr Cys Val Val Ser Gly Gly Ser Ile
W--> 154                270                275                280
156 AGC GGT TAC TAC TAC TGG ACC TGG ATC CGC CAG ACC CCA GGG AGG GGA     192
157 Ser Gly Tyr Tyr Tyr Trp Thr Trp Ile Arg Gln Thr Pro Gly Arg Gly
W--> 158                285                290                295
160 CTG GAG TGG ATT GGC CAT ATT TAT GGT AAT GGT GCG ACC ACC AAC TAC     240
161 Leu Glu Trp Ile Gly His Ile Tyr Gly Asn Gly Ala Thr Thr Asn Tyr
W--> 162 300                305                310                315
164 AAT CCC TCC CTC AAG AGT CGA GTC ACC ATT TCA AAA GAC ACG TCC AAG     288
165 Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Lys Asp Thr Ser Lys
W--> 166                320                325                330
168 AAC CAG TTC TTC CTG AAC TTG AAT TCT GTG ACC GAC GCG GAC ACG GCC     336
169 Asn Gln Phe Phe Leu Asn Leu Asn Ser Val Thr Asp Ala Asp Thr Ala
W--> 170                335                340                345
172 GTC TAT TAC TGT GCG AGA GGC CCT CGC CCT GAT TGC ACA ACC ATT TGT     384
173 Val Tyr Tyr Cys Ala Arg Gly Pro Arg Pro Asp Cys Thr Thr Ile Cys
W--> 174                350                355                360
176 TAT GGC GGC TGG GTC GAT GTC TGG GGC CCG GGA GAC CTG GTC ACC GTC     432
177 Tyr Gly Gly Trp Val Asp Val Trp Gly Pro Gly Asp Leu Val Thr Val
W--> 178                365                370                375
180 TCC TCA GCT AGC ACC AAG GGC CCA TCG GTC TTC CCC CTG GCA CCC TCC     480
181 Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
W--> 182 380                385                390                395
184 TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC AAG     528
185 Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
W--> 186                400                405                410
188 GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG     576
189 Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
W--> 190                415                420                425
192 ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC     624

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	193	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	
W-->	194			430				435					440					
	196	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	672
	197	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	
W-->	198			445				450					455					
	200	CAG	ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	720
	201	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	
W-->	202	460					465					470				475		
	204	GAC	AAG	AAA	GCA	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	768
	205	Asp	Lys	Lys	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	
W-->	206					480					485				490			
	208	CCG	TGC	CCA	GCA	CCT	GAA	CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	CTC	TTC	816
	209	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	
W-->	210				495				500					505				
	212	CCC	CCA	AAA	CCC	AAG	GAC	ACC	CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	864
	213	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	
W-->	214			510				515					520					
	216	ACA	TGC	GTG	GTG	GTG	GAC	GTG	AGC	CAC	GAA	GAC	CCT	GAG	GTC	AAG	TTC	912
	217	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	
W-->	218			525				530					535					
	220	AAC	TGG	TAC	GTG	GAC	GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	CCG	960
	221	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	
W-->	222	540				545					550				555			
	224	CGG	GAG	GAG	CAG	TAC	AAC	AGC	ACG	TAC	CGT	GTG	GTC	AGC	GTC	CTC	ACC	1008
	225	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	
W-->	226				560						565				570			
	228	GTC	CTG	CAC	CAG	GAC	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	AAG	GTC	1056
	229	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	
W-->	230			575				580					585					
	232	TCC	AAC	AAA	GCC	CTC	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	1104
	233	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	
W-->	234			590				595					600					
	236	AAA	GGG	CAG	CCC	CGA	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	1152
	237	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	
W-->	238			605				610					615					
	240	GAT	GAG	CTG	ACC	AAG	AAC	CAG	GTC	AGC	CTG	ACC	TGC	CTG	GTC	AAA	GGC	1200
	241	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	
W-->	242	620				625					630				635			
	244	TTC	TAT	CCC	AGC	GAC	ATC	GCC	GTG	GAG	TGG	GAG	AGC	AAT	GGG	CAG	CCG	1248
	245	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	
W-->	246				640						645				650			
	248	GAG	AAC	AAC	TAC	AAG	ACC	ACG	CCT	CCC	GTG	CTG	GAC	TCC	GAC	GGC	TCC	1296
	249	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	
W-->	250			655				660					665					
	252	TTC	TTC	CTC	TAC	AGC	AAG	CTC	ACC	GTG	GAC	AAG	AGC	AGG	TGG	CAG	CAG	1344
	253	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	
W-->	254			670				675					680					
	256	GGG	AAC	GTC	TTC	TCA	TGC	TCC	GTG	ATG	CAT	GAG	GCT	CTG	CAC	AAC	CAC	1392
	257	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	

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W--> 258      685              690              695
      260 TAC ACG CAG AAG AGC CTC TCC CTG TCT CCG GGT AAA TGA      1431
      261 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys *
W--> 262 700              705              710
      265 (2) INFORMATION FOR SEQ ID NO: 3:
      267 (i) SEQUENCE CHARACTERISTICS:
      268 (A) LENGTH: 720 base pairs
      269 (B) TYPE: nucleic acid
      270 (C) STRANDEDNESS: single
      271 (D) TOPOLOGY: linear
      273 (ii) MOLECULE TYPE: DNA (genomic)
      275 (ix) FEATURE:
      276 (A) NAME/KEY: CDS
      277 (B) LOCATION: 1..720
      279 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
      281 ATG AGC CTC CCT GCT CAG CTC CTC GGG CTG CTA TTG CTC TGC GTC CCC      48
      282 Met Ser Leu Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Cys Val Pro
W--> 283      480      485      490
      285 GGG TCC AGT GGG GAA GTT GTG ATG ACT CAG TCT CCA CTG TCC CTT CCC      96
      286 Gly Ser Ser Gly Glu Val Met Thr Gln Ser Pro Leu Ser Leu Pro
W--> 287      495      500      505
      289 ATC ACA CCT GGA GAG CCG GCC TCC ATC TCC TGT AGG TCT AGT CAA AGC      144
      290 Ile Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
W--> 291 510      515      520      525
      293 CTT AAA CAC AGT AAT GGA GAC ACC TTC CTG AGT TGG TAT CAG CAG AAG      192
      294 Leu Lys His Ser Asn Gly Asp Thr Phe Leu Ser Trp Tyr Gln Gln Lys
W--> 295      530      535      540
      297 CCA GGC CAA CCT CCA AGG CTC CTG ATT TAT AAG GTT TCT AAC CGG GAC      240
      298 Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Asp
W--> 299      545      550      555
      301 TCT GGG GTC CCA GAC AGA TTC AGC GGC AGT GGG GCA GGG ACA GAT TTC      288
      302 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe
W--> 303      560      565      570
      305 ACA CTG AAA ATC AGC GCA GTG GAG GCT GAA GAT GTT GGG GTT TAT TTC      336
      306 Thr Leu Lys Ile Ser Ala Val Glu Ala Glu Asp Val Gly Val Tyr Phe
W--> 307      575      580      585
      309 TGC GGG CAA GGT ACA AGG ACT CCT CCC ACT TTC GGC GGA GGG ACC AAG      384
      310 Cys Gly Gln Gly Thr Arg Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys
W--> 311 590      595      600      605
      313 GTG GAA ATC AAA CGT ACG GTG GCT GCA CCA TCT GTC TTC ATC TTC CCG      432
      314 Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
W--> 315      610      615      620
      317 CCA TCT GAT GAG CAG TTG AAA TCT GGA ACT GCC TCT GTT GTG TGC CTG      480
      318 Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
W--> 319      625      630      635
      321 CTG AAT AAC TTC TAT CCC AGA GAG GCC AAA GTA CAG TGG AAG GTG GAT      528
      322 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
W--> 323      640      645      650
      325 AAC GCC CTC CAA TCG GGT AAC TCC CAG GAG AGT GTC ACA GAG CAG GAC      576

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Input Set : N:\Crf3\RULE60\10073138.raw

Output Set: N:\CRF3\07252002\J073138.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:125 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:150 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:154 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:158 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:162 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:166 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
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L:178 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
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L:194 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:202 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:206 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
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L:218 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:222 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:226 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:230 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:234 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:238 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:242 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:246 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:250 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:254 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:258 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:262 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:283 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:287 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
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L:319 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:323 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:327 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:331 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:335 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:339 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3

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L:360 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:364 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:368 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:372 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4